

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	4	krix1 or (krix adj "1") or (lmbp adj 5089CB) or (lmbp5089cb)	USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:44
L2	6	krix1 or (krix adj "1") or (lmbp adj 5089CB) or (lmbp5089cb)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:44
L3	10886	fviii or fviiia or (factor adj (viii or viiia or eight)) or factor-viii or factor-viia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L4	257464	antibody or antibodies or immunoglobulin or immunoglobulins or immunoadhesin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L5	35511	sirs or sepsis or (systemic adj inflammatory adj response adj syndrome) or dic	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L6	581945	c1	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L7	259	(L3 same L4) and L5	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:45
L8	22	L7 and L6	USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L9	62	L7 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L10	216	jacquemin.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:46
L11	40	(saint-remy.in.) or (saintremy.in.) or ((saint adj remy).in.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:47
L12	34	(l10 or l11) and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/09/05 12:48

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rag.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:42:08 ; Search time 115.35 Seconds  
(without alignments)  
618.341 Million cell updates/sec

Title: US-10-044-569B-6  
Perfect score: 837  
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GYTSHYFDYWGRGTLVTSS 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
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2: geneseqp1990s:\*  
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9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	837	100.0	156	4	AAB47059	Aab47059 Heavy cha
2	837	100.0	156	5	AAO18878	Aao18878 Human KRI
3	837	100.0	165	9	ADY34082	Ady34082 Factor VI
4	735	87.8	288	9	ADY34106	Ady34106 Factor VI
5	611.5	73.1	471	7	ADE28427	Ade28427 Human ant
6	607	72.5	470	5	AAU74296	Aau74296 Anti-huma
7	602	71.9	141	9	ADY16604	Ady16604 PRO polyp
8	599.5	71.6	576	8	ADF69325	Adf69325 Human lun
9	587.5	70.2	139	9	ADX98261	Adx98261 Human ant
10	586	70.0	146	2	AAW22841	Aaw22841 Human ant
11	574.5	68.6	139	9	ADX98257	Adx98257 Human ant
12	550.5	65.8	236	4	AAB36215	Aab36215 Human imm
13	550	65.7	117	2	AAR66296	Aar66296 Human imm
14	547.5	65.4	148	3	AAV96295	Aay96295 Human IGF
15	547.5	65.4	198	8	ADF69324	Adf69324 Human lun
16	544.5	65.1	145	6	ABP57367	Abp57367 Anti-TRAI
17	540.5	64.6	146	3	AAB53510	Aab53510 Human col
18	540	64.5	476	2	AAW88464	Aaw88464 Monoclonal
19	539	64.4	250	5	ABP45711	Abp45711 Human BLY
20	539	64.4	250	7	ADG96538	Adg96538 Single ch
21	539	64.4	250	9	AED78591	Aed78591 Human B L
22	537	64.2	134	9	ADZ57712	Adz57712 Germline
23	536	64.0	136	9	ADZ57729	Adz57729 Anti-cMet
24	532	63.6	136	9	ADZ57728	Adz57728 Anti-cMet
25	532	63.6	149	2	AAV24370	Aay24370 Human mon
26	532	63.6	172	8	ADK52436	Adk52436 Human ant
27	531	63.4	136	9	ADZ57732	Adz57732 Anti-cMet
28	530	63.3	464	9	AEA41032	Aea41032 Human ant
29	529.5	63.3	746	4	AAU31804	Aau31804 Novel hum
30	528.5	63.1	135	3	AAV80290	Aay80290 Humanised
31	528.5	63.1	281	8	ADP03813	Adp03813 Human ant
32	528.5	63.1	286	8	ADP03811	Adp03811 Human ant
33	528	63.1	136	9	ADZ57727	Adz57727 Anti-cMet
34	527.5	63.0	135	3	AAV80289	Aay80289 Humanised
35	527	63.0	136	9	ADZ57731	Adz57731 Anti-cMet
36	527	63.0	250	5	ABP45712	Abp45712 Human BLY
37	527	63.0	250	7	ADG96539	Adg96539 Single ch
38	527	63.0	250	9	AED78592	Aed78592 Human B L
39	525.5	62.8	146	2	AAV24372	Aay24372 Human mon
40	525.5	62.8	256	5	ABP45629	Abp45629 Human BLY
41	525.5	62.8	256	7	ADG96456	Adg96456 Single ch
42	525.5	62.8	256	9	AED78509	Aed78509 Human B L
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44	523.5	62.5	139	2	AAW62204	Aaw62204 Humanised
45	523.5	62.5	139	2	AAV02570	Aay02570 Humanised

## ALIGNMENTS

## RESULT 1

AAB47059

ID AAB47059 standard; protein; 156 AA.

XX

AC AAB47059;

XX

DT 08-MAY-2001 (first entry)

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.ra1.

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This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-6.ra1.

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:59:49 ; Search time 30.3553 Seconds  
(without alignments)  
449.831 Million cell updates/sec

Title: US-10-044-569B-6  
Perfect score: 837  
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GYTSHYFDYWGRGTLTVSS 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	%				
No.	Score	Match	Length	ID		Description

1	607	72.5	470	2	US-09-859-053-28	Sequence 28, Appl
2	550.5	65.8	236	2	US-09-049-672A-13	Sequence 13, Appl
3	550	65.7	117	2	US-08-545-809A-90	Sequence 90, Appl
4	550	65.7	117	2	US-09-515-697-90	Sequence 90, Appl
5	532	63.6	149	2	US-09-582-337-8	Sequence 8, Appli
6	525.5	62.8	146	2	US-09-582-337-12	Sequence 12, Appl
7	525	62.7	140	1	US-07-946-421-28	Sequence 28, Appl
8	523.5	62.5	139	2	US-09-269-921-123	Sequence 123, App
9	523.5	62.5	146	2	US-09-582-337-10	Sequence 10, Appl
10	520.5	62.2	135	1	US-08-137-117D-112	Sequence 112, App
11	520.5	62.2	135	1	US-08-436-717-112	Sequence 112, App
12	519.5	62.1	139	2	US-09-269-921-108	Sequence 108, App
13	519.5	62.1	139	2	US-09-269-921-115	Sequence 115, App
14	518.5	61.9	139	2	US-09-269-921-124	Sequence 124, App
15	517.5	61.8	137	2	US-08-513-968-38	Sequence 38, Appl
16	517.5	61.8	139	2	US-09-355-925-7	Sequence 7, Appli
17	517.5	61.8	139	2	US-09-269-921-121	Sequence 121, App
18	517.5	61.8	139	2	US-09-269-921-125	Sequence 125, App
19	516.5	61.7	139	2	US-09-269-921-109	Sequence 109, App
20	516.5	61.7	139	2	US-09-269-921-118	Sequence 118, App
21	516	61.6	123	1	US-08-477-877B-94	Sequence 94, Appl
22	516	61.6	123	1	US-08-472-281A-94	Sequence 94, Appl
23	516	61.6	123	1	US-08-477-989B-94	Sequence 94, Appl
24	516	61.6	123	2	US-09-462-140D-102	Sequence 102, App
25	516	61.6	123	2	US-09-462-140D-105	Sequence 105, App
26	515.5	61.6	139	2	US-09-269-921-113	Sequence 113, App
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31	514.5	61.5	139	2	US-09-269-921-116	Sequence 116, App
32	514.5	61.5	139	2	US-09-269-921-119	Sequence 119, App
33	513.5	61.4	139	2	US-09-355-925-8	Sequence 8, Appli
34	513.5	61.4	139	2	US-09-269-921-110	Sequence 110, App
35	513.5	61.4	139	2	US-09-269-921-128	Sequence 128, App
36	512.5	61.2	135	1	US-08-137-117D-100	Sequence 100, App
37	512.5	61.2	135	1	US-08-436-717-100	Sequence 100, App
38	512.5	61.2	139	2	US-09-269-921-112	Sequence 112, App
39	512.5	61.2	139	2	US-09-269-921-117	Sequence 117, App
40	510.5	61.0	139	2	US-09-269-921-111	Sequence 111, App
41	510.5	61.0	139	2	US-09-269-921-120	Sequence 120, App
42	509	60.8	142	1	US-08-561-521-17	Sequence 17, Appl
43	509	60.8	142	5	PCT-US95-01219-17	Sequence 17, Appl
44	508	60.7	470	2	US-09-499-662-157	Sequence 157, App
45	506.5	60.5	467	1	US-07-916-098A-45	Sequence 45, Appl

## ALIGNMENTS

## RESULT 1

US-09-859-053-28

; Sequence 28, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

http://es/ScoreAccessWeb/GetItem.action?AppId=10044569&seqId=580481&ItemName=us-... 9/5/06

1	837	100.0	156	4	US-10-044-569B-6	Sequence 6, Appli
2	611.5	73.1	471	4	US-10-292-088-46	Sequence 46, Appl
3	607	72.5	470	3	US-09-859-053-28	Sequence 28, Appl
4	607	72.5	470	4	US-10-800-250-28	Sequence 28, Appl
5	607	72.5	470	4	US-10-625-105-28	Sequence 28, Appl
6	587.5	70.2	139	5	US-10-893-576-33	Sequence 33, Appl
7	574.5	68.6	139	5	US-10-893-576-29	Sequence 29, Appl
8	544.5	65.1	145	4	US-10-478-056-29	Sequence 29, Appl
9	544.5	65.1	145	5	US-10-721-763-29	Sequence 29, Appl
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11	540.5	64.6	146	3	US-09-925-299-1050	Sequence 1050, Ap
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20	532	63.6	172	5	US-10-644-277-142	Sequence 142, App
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22	527	63.0	250	3	US-09-880-748-1723	Sequence 1723, Ap
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26	525.5	62.8	146	4	US-10-390-986-12	Sequence 12, Appl
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33	523.5	62.5	139	4	US-10-218-253-123	Sequence 123, App
34	523.5	62.5	139	6	US-11-226-325-46	Sequence 46, Appl
35	523.5	62.5	146	4	US-10-390-986-10	Sequence 10, Appl
36	522.5	62.4	432	4	US-10-389-223A-10	Sequence 10, Appl
37	522.5	62.4	480	4	US-10-389-223A-4	Sequence 4, Appli
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41	521.5	62.3	469	6	US-11-031-485-42	Sequence 42, Appl
42	521	62.2	462	5	US-10-910-901-2	Sequence 2, Appli
43	520.5	62.2	135	5	US-10-837-904-109	Sequence 109, App
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45	520.5	62.2	249	3	US-09-880-748-1635	Sequence 1635, Ap

## ALIGNMENTS

## RESULT 1

US-10-044-569B-6

; Sequence 6, Application US/10044569B

; Publication No. US20030175268A1

; GENERAL INFORMATION:

; APPLICANT: D. Collen Research Foundation vzw

; APPLICANT: Jacquemin, Marc G

; APPLICANT: Saint-Remy, Jean-Marie R

; TITLE OF INVENTION: Method and pharmaceutical composition for preventing

; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome

; FILE REFERENCE: C1968

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rapbn.

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM protein - protein search, using sw model

Run on: August 9, 2006, 02:27:00 ; Search time 15.3096 Seconds  
(without alignments)  
681.831 Million cell updates/sec

Title: US-10-044-569B-6  
Perfect score: 837  
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GYTSHYFDYWGRGTLTVSS 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	837	100.0	165	7	US-11-298-560-2	Sequence 2, Appli
2	735	87.8	288	7	US-11-298-560-26	Sequence 26, Appl
3	611.5	73.1	471	7	US-11-211-917-46	Sequence 46, Appl
4	530	63.3	464	7	US-11-375-221-22	Sequence 22, Appl
5	517.5	61.8	139	6	US-10-533-104A-21	Sequence 21, Appl
6	514.5	61.5	122	7	US-11-211-917-110	Sequence 110, App
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8	509	60.8	142	7	US-11-006-808-17	Sequence 17, Appl
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14	492.5	58.8	447	7	US-11-221-902-12	Sequence 12, Appl
15	490.5	58.6	477	7	US-11-293-697-4289	Sequence 4289, Ap
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18	482.5	57.6	120	7	US-11-221-902-18	Sequence 18, Appl
19	482.5	57.6	447	7	US-11-221-902-8	Sequence 8, Appli
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21	479.5	57.3	475	6	US-10-523-295-32	Sequence 32, Appl
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30	473.5	56.6	473	7	US-11-293-697-4284	Sequence 4284, Ap
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32	470	56.2	495	7	US-11-293-697-4277	Sequence 4277, Ap
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34	466	55.7	495	7	US-11-293-697-4085	Sequence 4085, Ap
35	463	55.3	476	7	US-11-293-697-4288	Sequence 4288, Ap
36	460.5	55.0	108	6	US-10-484-105-14	Sequence 14, Appl
37	460	55.0	129	7	US-11-006-808-45	Sequence 45, Appl
38	457	54.6	470	7	US-11-293-697-4292	Sequence 4292, Ap
39	456	54.5	143	7	US-11-224-664-26	Sequence 26, Appl
40	451	53.9	117	7	US-11-249-296-6	Sequence 6, Appli
41	451	53.9	124	6	US-10-981-300-49	Sequence 49, Appl
42	449	53.6	474	7	US-11-293-697-4282	Sequence 4282, Ap
43	447	53.4	118	7	US-11-375-221-111	Sequence 111, App
44	446.5	53.3	118	7	US-11-094-132-62	Sequence 62, Appl
45	446	53.3	98	7	US-11-221-902-52	Sequence 52, Appl

## ALIGNMENTS

## RESULT 1

US-11-298-560-2

; Sequence 2, Application US/11298560

; Publication No. US20060115474A1

; GENERAL INFORMATION:

; APPLICANT: Jacquemin, Marc

; APPLICANT: Saint-Remy, Jean-Marie

; TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment o

; TITLE OF INVENTION: Hemostasis Disorders

# SCORE Search Results Details for Application 100

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This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569B-6  
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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:50:34 ; Search time 18.7411 Seconds  
(without alignments)  
800.903 Million cell updates/sec

Title: US-10-044-569B-6  
Perfect score: 837  
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GYTSHYFDYWGRGTLVTVSS 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	606.5	72.5	135	2 S49530	anti-Sm antibody V
2	591.5	70.7	171	2 S23623	Ig heavy chain V r
3	550	65.7	117	2 S18551	Ig heavy chain V r
4	549.5	65.7	136	2 S31600	Ig heavy chain pre
5	548	65.5	117	1 HVHU35	Ig heavy chain V r
6	540	64.5	117	2 S31680	Ig heavy chain V r
7	523.5	62.5	132	2 S31596	Ig heavy chain V r
8	521	62.2	160	2 PL0105	anti-PR2 erythrocy

9	517	61.8	148	2	S29257	Ig heavy chain V r
10	515	61.5	142	2	S19245	Ig heavy chain pre
11	505	60.3	129	2	S46393	Ig heavy chain V r
12	502	60.0	123	2	D33548	Ig heavy chain V-1
13	498	59.5	142	2	A32483	Ig heavy chain V r
14	493	58.9	117	2	S18553	Ig heavy chain V r
15	491	58.7	134	2	S21916	Ig heavy chain V r
16	490.5	58.6	118	2	S36265	Ig heavy chain V r
17	489	58.4	627	2	S14683	Ig mu chain precur
18	486	58.1	117	1	HVHUHG	Ig heavy chain pre
19	482.5	57.6	143	1	E1HUND	Ig heavy chain pre
20	477	57.0	117	2	S18552	Ig heavy chain V r
21	474	56.6	131	2	S21924	Ig heavy chain V r
22	465	55.6	117	2	PT0371	Ig gamma chain pre
23	464.5	55.5	139	1	MHMS18	Ig heavy chain pre
24	462.5	55.3	137	2	C41287	Ig heavy chain pre
25	460	55.0	117	2	S18554	Ig heavy chain V r
26	456	54.5	138	1	HVMST7	Ig heavy chain pre
27	454	54.2	104	2	S69899	Ig heavy chain V r
28	453.5	54.2	110	2	PH1669	Ig heavy chain V r
29	450.5	53.8	135	2	A30577	Ig heavy chain pre
30	450	53.8	138	2	E32513	Ig heavy chain pre
31	447	53.4	111	2	S21925	Ig heavy chain V r
32	446	53.3	98	2	S26938	Ig heavy chain V r
33	443	52.9	121	2	S20783	Ig heavy chain V r
34	439.5	52.5	137	1	G2MS43	Ig heavy chain pre
35	438.5	52.4	116	2	S31698	Ig heavy chain pre
36	438	52.3	98	2	S26912	Ig heavy chain V r
37	438	52.3	109	2	PH1668	Ig heavy chain V r
38	437.5	52.3	137	2	F29380	Ig heavy chain pre
39	437.5	52.3	474	1	G2MS11	Ig gamma-2b chain
40	436.5	52.2	116	2	S31667	Ig heavy chain V r
41	435.5	52.0	137	2	H32513	Ig heavy chain pre
42	435	52.0	127	2	S34014	Ig heavy chain V r
43	434	51.9	126	2	I44151	Ig heavy chain V r
44	433.5	51.8	137	2	E29380	Ig heavy chain pre
45	433.5	51.8	469	2	S37483	Ig gamma-2a chain

## ALIGNMENTS

## RESULT 1

S49530

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999

C;Accession: S49530

R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.

A;Reference number: S48797.

A;Accession: S49530

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-135

A;Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:g560839; PIDN:CAA86467.1;

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology

Query Match

72.5%; Score 606.5; DB 2; Length 135;

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-6.rup.

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This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569b-6.rup.

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:43:08 ; Search time 145.706 Seconds  
(without alignments)  
990.370 Million cell updates/sec

Title: US-10-044-569B-6  
Perfect score: 837  
Sequence: 1 MDWTWRILFLVAAATGAHSQ.....GYTSHYFDYWGRGTLTVSS 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	548	65.5	117	1	HV1G_HUMAN	P23083 homo sapien
2	533.5	63.7	498	2	Q6N041_HUMAN	Q6n041 homo sapien
3	528.5	63.1	518	2	Q6N030_HUMAN	Q6n030 homo sapien
4	520	62.1	480	2	Q6P089_HUMAN	Q6p089 homo sapien

5	511	61.1	519	2	Q5EBM2_HUMAN	Q5ebm2	homo sapien
6	509	60.8	497	2	Q8WY24_HUMAN	Q8wy24	homo sapien
7	503.5	60.2	500	2	Q9BRV0_HUMAN	Q9brv0	homo sapien
8	502	60.0	500	2	Q6N091_HUMAN	Q6n091	homo sapien
9	493.5	59.0	469	2	Q7Z7P5_HUMAN	Q7z7p5	homo sapien
10	493	58.9	150	2	Q9Y298_HUMAN	Q9y298	homo sapien
11	489.5	58.5	147	1	HV1C_HUMAN	P01744	homo sapien
12	489.5	58.5	159	2	Q96QS0_HUMAN	Q96qs0	homo sapien
13	486	58.1	117	1	HV1B_HUMAN	P01743	homo sapien
14	476	56.9	119	2	Q9UL94_HUMAN	Q9ul94	homo sapien
15	476	56.9	125	2	Q9UL95_HUMAN	Q9ul95	homo sapien
16	475	56.8	157	2	O95978_HUMAN	O95978	homo sapien
17	467	55.8	208	2	Q6ZP87_HUMAN	Q6zp87	homo sapien
18	466.5	55.7	496	2	Q96DK0_HUMAN	Q96dk0	homo sapien
19	464.5	55.5	139	1	HV07_MOUSE	P01751	mus musculu
20	459.5	54.9	124	2	Q9UL92_HUMAN	Q9ul92	homo sapien
21	459.5	54.9	475	2	Q6N095_HUMAN	Q6n095	homo sapien
22	458	54.7	473	2	Q9D8L4_MOUSE	Q9d8l4	mus musculu
23	456	54.5	138	1	HV48_MOUSE	P03980	mus musculu
24	450	53.8	616	2	Q504M7_MOUSE	Q504m7	mus musculu
25	448	53.5	458	2	Q5BJZ2_RAT	Q5bjz2	rattus norv
26	446	53.3	244	2	Q65ZC8_HUMAN	Q65zc8	homo sapien
27	445.5	53.2	598	2	Q568Y0_RAT	Q568y0	rattus norv
28	444.5	53.1	613	2	Q8VCX7_MOUSE	Q8vcx7	mus musculu
29	444	53.0	480	2	Q6PJF1_HUMAN	Q6pjf1	homo sapien
30	442	52.8	120	2	Q6NSA4_HUMAN	Q6nsa4	homo sapien
31	441.5	52.7	463	2	Q99LC4_MOUSE	Q99lc4	mus musculu
32	441.5	52.7	482	2	Q8K172_MOUSE	Q8k172	mus musculu
33	441	52.7	468	2	Q569W9_MOUSE	Q569w9	mus musculu
34	440	52.6	168	2	Q8VDC9_MOUSE	Q8vdc9	mus musculu
35	439.5	52.5	137	1	HV11_MOUSE	P01755	mus musculu
36	437	52.2	477	2	Q569B1_RAT	Q569b1	rattus norv
37	435.5	52.0	484	2	Q3SYJ4_MOUSE	Q3syj4	mus musculu
38	433	51.7	475	2	Q5FVP3_RAT	Q5fvp3	rattus norv
39	432.5	51.7	591	2	Q4QQW0_RAT	Q4qqw0	rattus norv
40	432	51.6	506	2	Q6MZW0_HUMAN	Q6mzw0	homo sapien
41	430.5	51.4	488	2	Q8K0F2_MOUSE	Q8k0f2	mus musculu
42	428	51.1	483	2	Q4VAB6_MOUSE	Q4vab6	mus musculu
43	427.5	51.1	465	2	Q6PJB2_MOUSE	Q6pjb2	mus musculu
44	425.5	50.8	480	2	Q2NLC3_MOUSE	Q2nlc3	mus musculu
45	425	50.8	470	2	Q7TMK1_MOUSE	Q7tmk1	mus musculu

## ALIGNMENTS

## RESULT 1

HV1G\_HUMAN

ID HV1G\_HUMAN STANDARD; PRT; 117 AA.

AC P23083;

DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1991, sequence version 1.

DT 07-MAR-2006, entry version 36.

DE Ig heavy chain V-I region V35 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:42:08 ; Search time 105.738 Seconds  
(without alignments)  
618.341 Million cell updates/sec

Title: US-10-044-569B-8  
Perfect score: 738  
Sequence: 1 METPAQLLFLLLLWLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	738	100.0	143	4	AAB47061	Aab47061 Light cha
2	738	100.0	143	5	AAO18879	Aao18879 Human KRI
3	730	98.9	143	9	ADY34084	Ady34084 Factor VI
4	684.5	92.8	235	9	AEA41059	Aea41059 Anti-M-CS
5	680.5	92.2	235	9	AEA41041	Aea41041 Anti-M-CS
6	676.5	91.7	235	9	AEA41049	Aea41049 Anti-M-CS
7	667	90.4	234	7	ADE28481	Ade28481 Human ant
8	666.5	90.3	235	3	AAAY93702	Aay93702 The kappa
9	666.5	90.3	235	3	AAAY93729	Aay93729 The kappa
10	666.5	90.3	235	6	AAE35884	Aae35884 Human 4.1
11	666.5	90.3	235	9	AED04279	Aed04279 Human ant
12	666.5	90.3	235	9	AED04315	Aed04315 Human ant
13	664	90.0	288	9	ADY34106	Ady34106 Factor VI
14	662.5	89.8	236	10	AEF73710	Aef73710 Human IL-
15	660	89.4	236	5	AAU74299	Aau74299 Anti-huma
16	659	89.3	236	9	ADZ70600	Adz70600 Human pro
17	658.5	89.2	235	6	ABP71366	Abp71366 Anti-OPGL
18	655	88.8	236	9	ADZ57699	Adz57699 Anti-cMet
19	654.5	88.7	142	4	AAB47060	Aab47060 Light cha
20	654.5	88.7	142	5	AAO18877	Aao18877 Human B02
21	654.5	88.7	233	3	AAAY93704	Aay93704 The kappa
22	654.5	88.7	233	3	AAAY93731	Aay93731 The kappa
23	654.5	88.7	233	6	AAE35886	Aae35886 Human 4.8
24	654.5	88.7	233	9	AED04283	Aed04283 Human ant
25	654.5	88.7	233	9	AED04319	Aed04319 Human ant
26	653.5	88.6	235	9	AED14792	Aed14792 Ab D anti
27	652	88.3	236	5	AAU74301	Aau74301 Anti-huma
28	649.5	88.0	150	2	AAW40069	Aaw40069 Human mon
29	649.5	88.0	150	4	AAE00946	Aae00946 Human mon
30	649.5	88.0	150	8	ADO52287	Ado52287 Human ant
31	645	87.4	234	3	AAAY93733	Aay93733 The kappa
32	645	87.4	234	3	AAAY93708	Aay93708 The kappa
33	645	87.4	234	6	AAE35888	Aae35888 Human 6.1
34	645	87.4	234	9	AED04287	Aed04287 Human ant
35	645	87.4	234	9	AED04327	Aed04327 Human ant
36	641.5	86.9	150	7	ABU10485	Abu10485 Human C-a
37	633.5	85.8	239	8	ADK70470	Adk70470 Respirato
38	630.5	85.4	235	10	AAE86006	Aee86006 Anthrax t
39	629.5	85.3	235	8	ADM41573	Adm41573 Anti-inte
40	627	85.0	234	7	ADE28473	Ade28473 Human ant
41	623	84.4	236	9	ADZ51040	Adz51040 Amino aci
42	622	84.3	131	6	ABP57366	Abp57366 Anti-TRAI
43	619.5	83.9	130	6	ADA43061	Ada43061 Human ant
44	619.5	83.9	238	6	ABR41582	Abr41582 Human DIT
45	614	83.2	127	9	ADW76948	Adw76948 RGL C lig

## ALIGNMENTS

## RESULT 1

AAB47061

ID AAB47061 standard; protein; 143 AA.

XX

AC AAB47061;

XX

DT 08-MAY-2001 (first entry)





1	666.5	90.3	235	2	US-09-472-087-14	Sequence 14, Appl
2	666.5	90.3	235	2	US-09-472-087-65	Sequence 65, Appl
3	660	89.4	236	2	US-09-859-053-34	Sequence 34, Appl
4	654.5	88.7	233	2	US-09-472-087-15	Sequence 15, Appl
5	654.5	88.7	233	2	US-09-472-087-67	Sequence 67, Appl
6	652	88.3	236	2	US-09-859-053-38	Sequence 38, Appl
7	649.5	88.0	150	2	US-08-862-124-5	Sequence 5, Appli
8	645	87.4	234	2	US-09-472-087-17	Sequence 17, Appl
9	645	87.4	234	2	US-09-472-087-69	Sequence 69, Appl
10	604	81.8	134	1	US-08-405-034-4	Sequence 4, Appli
11	585	79.3	234	2	US-09-848-832-4	Sequence 4, Appli
12	583.5	79.1	129	1	US-08-480-774A-4	Sequence 4, Appli
13	575	77.9	226	2	US-09-456-090A-42	Sequence 42, Appl
14	575	77.9	226	2	US-09-453-234-42	Sequence 42, Appl
15	571	77.4	226	2	US-09-456-090A-50	Sequence 50, Appl
16	571	77.4	226	2	US-09-456-090A-86	Sequence 86, Appl
17	571	77.4	226	2	US-09-453-234-50	Sequence 50, Appl
18	571	77.4	226	2	US-09-453-234-86	Sequence 86, Appl
19	569	77.1	226	2	US-09-456-090A-80	Sequence 80, Appl
20	569	77.1	226	2	US-09-453-234-80	Sequence 80, Appl
21	567	76.8	224	2	US-09-456-090A-52	Sequence 52, Appl
22	567	76.8	224	2	US-09-453-234-52	Sequence 52, Appl
23	566	76.7	226	2	US-09-456-090A-72	Sequence 72, Appl
24	566	76.7	226	2	US-09-453-234-72	Sequence 72, Appl
25	564	76.4	116	1	US-08-053-131-183	Sequence 183, App
26	564	76.4	116	1	US-08-096-762-183	Sequence 183, App
27	564	76.4	116	2	US-09-042-353-46	Sequence 46, Appl
28	564	76.4	116	2	US-08-758-417A-311	Sequence 311, App
29	564	76.4	226	2	US-09-456-090A-38	Sequence 38, Appl
30	564	76.4	226	2	US-09-453-234-38	Sequence 38, Appl
31	560	75.9	234	2	US-09-049-672A-6	Sequence 6, Appli
32	559	75.7	226	2	US-09-456-090A-74	Sequence 74, Appl
33	559	75.7	226	2	US-09-453-234-74	Sequence 74, Appl
34	554	75.1	224	2	US-09-456-090A-76	Sequence 76, Appl
35	554	75.1	224	2	US-09-453-234-76	Sequence 76, Appl
36	553	74.9	224	2	US-09-456-090A-44	Sequence 44, Appl
37	553	74.9	224	2	US-09-456-090A-78	Sequence 78, Appl
38	553	74.9	224	2	US-09-453-234-44	Sequence 44, Appl
39	553	74.9	224	2	US-09-453-234-78	Sequence 78, Appl
40	552	74.8	238	2	US-09-499-662-107	Sequence 107, App
41	549	74.4	224	2	US-09-456-090A-40	Sequence 40, Appl
42	549	74.4	224	2	US-09-453-234-40	Sequence 40, Appl
43	545	73.8	235	2	US-08-812-586-16	Sequence 16, Appl
44	545	73.8	235	2	US-09-535-832A-17	Sequence 17, Appl
45	540	73.2	238	2	US-09-499-662-50	Sequence 50, Appl

## ALIGNMENTS

## RESULT 1

US-09-472-087-14

; Sequence 14, Application US/09472087

; Patent No. 6682736

## ; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

http://es/ScoreAccessWeb/GetItem.action?AppId=10044569&seqId=580489&ItemName=us... 9/5/06

1	738	100.0	143	4	US-10-044-569B-8	Sequence 8, Appli
2	684.5	92.8	235	5	US-10-938-353-60	Sequence 60, Appl
3	680.5	92.2	235	5	US-10-938-353-32	Sequence 32, Appl
4	676.5	91.7	235	5	US-10-938-353-44	Sequence 44, Appl
5	667	90.4	234	4	US-10-292-088-88	Sequence 88, Appl
6	666.5	90.3	235	4	US-10-153-382-7	Sequence 7, Appli
7	666.5	90.3	235	5	US-10-612-497-14	Sequence 14, Appl
8	666.5	90.3	235	5	US-10-612-497-65	Sequence 65, Appl
9	666.5	90.3	235	5	US-10-776-649-14	Sequence 14, Appl
10	666.5	90.3	235	5	US-10-776-649-65	Sequence 65, Appl
11	666.5	90.3	235	6	US-11-085-368-7	Sequence 7, Appli
12	666.5	90.3	235	6	US-11-085-368-43	Sequence 43, Appl
13	666.5	90.3	235	6	US-11-128-900-14	Sequence 14, Appl
14	666.5	90.3	235	6	US-11-128-900-65	Sequence 65, Appl
15	660	89.4	236	3	US-09-859-053-34	Sequence 34, Appl
16	660	89.4	236	4	US-10-800-250-34	Sequence 34, Appl
17	660	89.4	236	4	US-10-625-105-34	Sequence 34, Appl
18	658.5	89.2	235	4	US-10-180-648-4	Sequence 4, Appli
19	655	88.8	236	5	US-10-910-901-8	Sequence 8, Appli
20	654.5	88.7	142	4	US-10-044-569B-4	Sequence 4, Appli
21	654.5	88.7	233	4	US-10-153-382-11	Sequence 11, Appl
22	654.5	88.7	233	5	US-10-612-497-15	Sequence 15, Appl
23	654.5	88.7	233	5	US-10-612-497-67	Sequence 67, Appl
24	654.5	88.7	233	5	US-10-776-649-15	Sequence 15, Appl
25	654.5	88.7	233	5	US-10-776-649-67	Sequence 67, Appl
26	654.5	88.7	233	6	US-11-085-368-11	Sequence 11, Appl
27	654.5	88.7	233	6	US-11-085-368-47	Sequence 47, Appl
28	654.5	88.7	233	6	US-11-128-900-15	Sequence 15, Appl
29	654.5	88.7	233	6	US-11-128-900-67	Sequence 67, Appl
30	653.5	88.6	235	6	US-11-086-289-16	Sequence 16, Appl
31	652	88.3	236	3	US-09-859-053-38	Sequence 38, Appl
32	652	88.3	236	4	US-10-800-250-38	Sequence 38, Appl
33	652	88.3	236	4	US-10-625-105-38	Sequence 38, Appl
34	649.5	88.0	150	3	US-09-782-397-5	Sequence 5, Appli
35	649.5	88.0	150	4	US-10-651-453-5	Sequence 5, Appli
36	645	87.4	234	4	US-10-153-382-15	Sequence 15, Appl
37	645	87.4	234	5	US-10-612-497-17	Sequence 17, Appl
38	645	87.4	234	5	US-10-612-497-69	Sequence 69, Appl
39	645	87.4	234	5	US-10-776-649-17	Sequence 17, Appl
40	645	87.4	234	5	US-10-776-649-69	Sequence 69, Appl
41	645	87.4	234	6	US-11-085-368-15	Sequence 15, Appl
42	645	87.4	234	6	US-11-085-368-55	Sequence 55, Appl
43	645	87.4	234	6	US-11-128-900-17	Sequence 17, Appl
44	645	87.4	234	6	US-11-128-900-69	Sequence 69, Appl
45	629.5	85.3	235	4	US-10-656-769-38	Sequence 38, Appl

## ALIGNMENTS

## RESULT 1

US-10-044-569B-8

; Sequence 8, Application US/10044569B

; Publication No. US20030175268A1

; GENERAL INFORMATION:

; APPLICANT: D. Collen Research Foundation vzw

; APPLICANT: Jacquemin, Marc G

; APPLICANT: Saint-Remy, Jean-Marie R

; TITLE OF INVENTION: Method and pharmaceutical composition for preventing

; TITLE OF INVENTION: and/or treating systemic inflammatory response syndrome

; FILE REFERENCE: C1968

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rapbn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM protein - protein search, using sw model

Run on: August 9, 2006, 02:27:00 ; Search time 14.0338 Seconds  
(without alignments)  
681.831 Million cell updates/sec

Title: US-10-044-569B-8  
Perfect score: 738  
Sequence: 1 METPAQLLFLLLLWLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	730	98.9	143	7	US-11-298-560-4	Sequence 4, Appli
2	684.5	92.8	235	7	US-11-375-221-60	Sequence 60, Appl
3	680.5	92.2	235	7	US-11-375-221-32	Sequence 32, Appl
4	676.5	91.7	235	7	US-11-375-221-44	Sequence 44, Appl
5	667	90.4	234	7	US-11-211-917-88	Sequence 88, Appl
6	664	90.0	288	7	US-11-298-560-26	Sequence 26, Appl
7	654.5	88.7	142	7	US-11-298-560-48	Sequence 48, Appl
8	627	85.0	234	7	US-11-211-917-72	Sequence 72, Appl
9	571	77.4	234	7	US-11-375-221-12	Sequence 12, Appl
10	523.5	70.9	223	7	US-11-365-556-305	Sequence 305, App
11	513.5	69.6	109	7	US-11-375-221-114	Sequence 114, App
12	500	67.8	214	6	US-10-515-429-75	Sequence 75, Appl
13	495.5	67.1	130	7	US-11-293-697-4264	Sequence 4264, Ap
14	494	66.9	234	7	US-11-211-917-24	Sequence 24, Appl
15	493.5	66.9	108	7	US-11-211-917-113	Sequence 113, App
16	491	66.5	107	7	US-11-211-917-84	Sequence 84, Appl
17	491	66.5	234	6	US-10-511-436A-92	Sequence 92, Appl
18	490	66.4	214	6	US-10-515-429-72	Sequence 72, Appl
19	487	66.0	234	7	US-11-211-917-48	Sequence 48, Appl
20	486	65.9	222	7	US-11-365-556-307	Sequence 307, App
21	484	65.6	236	7	US-11-375-221-20	Sequence 20, Appl
22	482.5	65.4	110	7	US-11-254-679-34	Sequence 34, Appl
23	481	65.2	236	7	US-11-375-221-52	Sequence 52, Appl
24	479.5	65.0	109	6	US-10-994-679-70	Sequence 70, Appl
25	479	64.9	234	7	US-11-375-221-4	Sequence 4, Appli
26	478	64.8	234	6	US-10-546-594-132	Sequence 132, App
27	478	64.8	234	7	US-11-375-221-8	Sequence 8, Appli
28	478	64.8	236	7	US-11-375-221-36	Sequence 36, Appl
29	474	64.2	236	7	US-11-375-221-16	Sequence 16, Appl
30	473.5	64.2	110	7	US-11-304-986-16	Sequence 16, Appl
31	473	64.1	238	7	US-11-298-020-10	Sequence 10, Appl
32	471	63.8	236	7	US-11-375-221-56	Sequence 56, Appl
33	468	63.4	236	7	US-11-375-221-48	Sequence 48, Appl
34	467.5	63.3	108	6	US-10-821-930-21	Sequence 21, Appl
35	467	63.3	214	7	US-11-254-182-40	Sequence 40, Appl
36	466	63.1	128	7	US-11-290-687-8	Sequence 8, Appli
37	466	63.1	171	6	US-10-981-300-10	Sequence 10, Appl
38	466	63.1	236	7	US-11-375-221-28	Sequence 28, Appl
39	464.5	62.9	109	6	US-10-994-679-62	Sequence 62, Appl
40	464	62.9	240	7	US-11-375-221-24	Sequence 24, Appl
41	463	62.7	236	7	US-11-290-687-25	Sequence 25, Appl
42	461	62.5	236	7	US-11-290-687-27	Sequence 27, Appl
43	460	62.3	107	7	US-11-211-917-100	Sequence 100, App
44	459	62.2	96	7	US-11-221-902-67	Sequence 67, Appl
45	459	62.2	96	7	US-11-239-308-51	Sequence 51, Appl

## ALIGNMENTS

## RESULT 1

US-11-298-560-4

; Sequence 4, Application US/11298560

; Publication No. US20060115474A1

; GENERAL INFORMATION:

; APPLICANT: Jacquemin, Marc

; APPLICANT: Saint-Remy, Jean-Marie

; TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment o

; TITLE OF INVENTION: Hemostasis Disorders

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This page gives you Search Results detail for the Application 10044569 and Search Result us-10-044-569B-8  
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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:50:34 ; Search time 17.1794 Seconds  
 (without alignments)  
 800.903 Million cell updates/sec

Title: US-10-044-569B-8  
 Perfect score: 738  
 Sequence: 1 METPAQLLFLLLWLPDTTG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	625.5	84.8	145	2 S20631	Ig kappa chain - h
2	619	83.9	144	2 PL0106	Ig kappa chain pre
3	608.5	82.5	129	1 K3HUHA	Ig kappa chain pre
4	598.5	81.1	129	1 K3HUHI	Ig kappa chain pre
5	596.5	80.8	129	2 S49532	anti-Sm antibody V
6	590.5	80.0	128	2 S20636	Ig kappa chain V r
7	585.5	79.3	129	2 S46369	IG light chain var
8	585.5	79.3	134	2 S38643	Ig kappa chain V r

9	576	78.0	129	2	S40325	Ig kappa chain - h
10	572.5	77.6	129	2	A32274	Ig kappa chain pre
11	570.5	77.3	130	2	S20637	Ig kappa chain V r
12	569	77.1	131	2	S40346	Ig kappa chain V-J
13	566.5	76.8	130	2	S40360	Ig kappa chain - h
14	564	76.4	116	2	B27594	Ig kappa chain pre
15	563.5	76.4	121	2	S40327	Ig kappa chain - h
16	552.5	74.9	116	2	C27594	Ig kappa chain pre
17	548.5	74.3	124	2	S20633	Ig kappa chain - h
18	537	72.8	116	2	B25521	Ig kappa chain pre
19	535	72.5	128	1	K3HU41	Ig kappa chain pre
20	533.5	72.3	127	2	S40380	Ig kappa chain V-J
21	533.5	72.3	129	2	S40363	Ig kappa chain - h
22	532.5	72.2	215	2	A23746	Ig kappa chain V-I
23	531	72.0	129	2	S29627	Ig kappa chain V r
24	527	71.4	128	2	S40379	Ig kappa chain V-J
25	526	71.3	114	2	S46375	Ig kappa chain V-J
26	525	71.1	125	2	S40344	Ig kappa chain V-J
27	525	71.1	128	2	S40345	Ig kappa chain V-J
28	524	71.0	128	2	A56701	Ig kappa chain V r
29	519.5	70.4	215	2	JE0242	Ig kappa chain NIG
30	518	70.2	128	2	S40343	Ig kappa chain V-J
31	510.5	69.2	109	2	A30608	Ig kappa chain V-I
32	510.5	69.2	131	2	S40328	Ig kappa chain - h
33	506.5	68.6	115	1	K3HUVG	Ig kappa chain pre
34	506.5	68.6	215	2	JE0244	Ig kappa chain NIG
35	505.5	68.5	109	2	B30601	Ig kappa chain V-I
36	503	68.2	116	1	K3HUVH	Ig kappa chain pre
37	503	68.2	116	2	S41817	Ig kappa chain V r
38	502.5	68.1	109	2	C30601	Ig kappa chain V-I
39	501.5	68.0	109	2	G30607	Ig kappa chain V-I
40	501	67.9	110	2	E30607	Ig kappa chain V-I
41	501	67.9	111	2	S40359	Ig kappa chain V-J
42	499.5	67.7	109	2	D30601	Ig kappa chain V-I
43	499	67.6	108	2	H44151	Ig kappa chain V r
44	497.5	67.4	109	2	H30601	Ig kappa chain V-I
45	494.5	67.0	109	2	G30601	Ig kappa chain V-I

## ALIGNMENTS

## RESULT 1

S20631

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C;Accession: S20631

R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A;Reference number: S20631

A;Accession: S20631

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-145

A;Cross-references: UNIPARC:UPI00001163DD; EMBL:Z11903; NID:g33156; PIDN:CAA77955.1; P

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-111/Domain: immunoglobulin homology

Query Match 84.8%; Score 625.5; DB 2; Length 145;

# SCORE Search Results Details for Application 10044569 and Search Result us-10-044-569b-8.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 01:43:08 ; Search time 133.563 Seconds  
(without alignments)  
990.370 Million cell updates/sec

Title: US-10-044-569B-8  
Perfect score: 738  
Sequence: 1 METPAQLLFLLLLWLPDITG.....TKVEIKRTVAAPSVFIFPPS 143

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	669	90.7	236	2 Q6P5S8_HUMAN	Q6p5s8 homo sapien
2	659	89.3	236	2 Q6PIL8_HUMAN	Q6pil8 homo sapien
3	642.5	87.1	235	2 Q6GMV9_HUMAN	Q6gmv9 homo sapien
4	639.5	86.7	235	2 Q6PJF2_HUMAN	Q6pjf2 homo sapien



5	608.5	82.5	129	1	KV3L_HUMAN	P18135	homo sapien
6	598.5	81.1	129	1	KV3M_HUMAN	P18136	homo sapien
7	586.5	79.5	235	2	Q6GMW0_HUMAN	Q6gmw0	homo sapien
8	575	77.9	234	2	Q569I9_HUMAN	Q569i9	homo sapien
9	535	72.5	128	1	KV3K_HUMAN	P06311	homo sapien
10	531.5	72.0	129	1	KV3H_HUMAN	P04207	homo sapien
11	506.5	68.6	115	1	KV3I_HUMAN	P04433	homo sapien
12	505.5	68.5	109	2	Q9UL78_HUMAN	Q9ul78	homo sapien
13	503	68.2	116	1	KV3J_HUMAN	P04434	homo sapien
14	498	67.5	236	2	Q6PIH7_HUMAN	Q6pih7	homo sapien
15	489.5	66.3	109	1	KV3B_HUMAN	P01620	homo sapien
16	489.5	66.3	109	1	KV3E_HUMAN	P01623	homo sapien
17	486	65.9	236	2	Q6GMX8_HUMAN	Q6gmx8	homo sapien
18	483.5	65.5	109	2	Q9UL86_HUMAN	Q9ul86	homo sapien
19	481.5	65.2	109	1	KV3D_HUMAN	P01622	homo sapien
20	479	64.9	234	2	Q7Z473_HUMAN	Q7z473	homo sapien
21	473	64.1	236	2	Q6PIH4_HUMAN	Q6pih4	homo sapien
22	473	64.1	236	2	Q6PIT5_HUMAN	Q6pit5	homo sapien
23	471	63.8	236	2	Q6GMX0_HUMAN	Q6gmx0	homo sapien
24	470	63.7	236	2	Q6GMW1_HUMAN	Q6gmw1	homo sapien
25	468	63.4	236	2	Q6GMX9_HUMAN	Q6gmx9	homo sapien
26	464.5	62.9	109	1	KV3G_HUMAN	P04206	homo sapien
27	461	62.5	236	2	Q502W4_HUMAN	Q502w4	homo sapien
28	460.5	62.4	239	2	Q8NEK0_HUMAN	Q8nek0	homo sapien
29	459	62.2	240	2	Q6PIH6_HUMAN	Q6pih6	homo sapien
30	457.5	62.0	108	1	KV3A_HUMAN	P01619	homo sapien
31	457	61.9	234	2	Q5EFE6_HUMAN	Q5efe6	homo sapien
32	456	61.8	100	1	KV3C_HUMAN	P01621	homo sapien
33	456	61.8	189	2	Q569I7_HUMAN	Q569i7	homo sapien
34	455	61.7	236	2	Q7Z3Y4_HUMAN	Q7z3y4	homo sapien
35	446	60.4	240	2	Q52L64_MOUSE	Q52l64	mus musculu
36	443.5	60.1	239	2	Q8TCD0_HUMAN	Q8tcd0	homo sapien
37	437	59.2	238	2	Q66JS7_MOUSE	Q66js7	mus musculu
38	436.5	59.1	109	2	Q9UL85_HUMAN	Q9ul85	homo sapien
39	422.5	57.2	109	1	KV3F_HUMAN	P01624	homo sapien
40	421	57.0	238	2	Q58EU4_MOUSE	Q58eu4	mus musculu
41	419.5	56.8	239	2	Q6P491_HUMAN	Q6p491	homo sapien
42	418	56.6	237	2	Q7SZ36_XENLA	Q7sz36	xenopus lae
43	417.5	56.6	133	1	KV4B_HUMAN	P06313	homo sapien
44	411	55.7	108	2	Q9UL83_HUMAN	Q9ul83	homo sapien
45	409.5	55.5	239	2	Q58EU8_MOUSE	Q58eu8	mus musculu

## ALIGNMENTS

## RESULT 1

Q6P5S8\_HUMAN

ID Q6P5S8\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6P5S8;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.